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RAW SEQUENCE LISTING

DATE: 08/23/2004

PATENT APPLICATION: US/10/714,161A

TIME: 15:40:49

Input Set : A:\Sequence Listing.TXT

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3 <110> APPLICANT: Carlton, Mark
4   Aparicio, Samuel
5   Dixon, John
6   Thresher, Rosemary
7   Zahn, Dirk
9 <120> TITLE OF INVENTION: Receptor
11 <130> FILE REFERENCE: 674580-2004
13 <140> CURRENT APPLICATION NUMBER: US 10/714,161A
14 <141> CURRENT FILING DATE: 2003-11-14
16 <150> PRIOR APPLICATION NUMBER: PCT/GB02/02304
17 <151> PRIOR FILING DATE: 2002-05-16
19 <150> PRIOR APPLICATION NUMBER: GB 0111959.3
20 <151> PRIOR FILING DATE: 2001-05-16
22 <150> PRIOR APPLICATION NUMBER: US 60/292,141
23 <151> PRIOR FILING DATE: 2001-05-18
25 <160> NUMBER OF SEQ ID NOS: 32
27 <170> SOFTWARE: PatentIn Ver. 2.1
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30 <211> LENGTH: 1478
31 <212> TYPE: DNA
32 <213> ORGANISM: Homo sapiens
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37 cctgccgacc ttagtttcaa agcttattct taattagaga caagaaacct gtttcaactt 180
38 gaagacaccg tatgaggtga atggacagcc agccaccaca atgaaagaaa tcaaaccagg 240
39 aataacctat gctgaaccca cgcctcaatc gtccccaagt gtttcttgac acgcatcttt 300
40 gcttacagtg catcacaact gaagaatggg gttcaacttg acgcttgcaa aattacaaaa 360
41 taacgagctg cacggccaag agagtcacaa ttcaggcaac aggagcgacg ggccaggaaa 420
42 gaacaccacc cttcacaatg aatttgacac aattgtcttg ccggtgcttt atctcattat 480
43 atttgtggca agcatcttgc tgaatggttt agcagtgtgg atcttcttcc acattaggaa 540
44 taaaaccagc ttcataattc atctcaaaaa catagtgtgt gcagacctca taatgacgct 600
45 gacatttcca tttcgaatag tccatgatgc aggatttgga ccttggtact tcaagtttat 660
46 tctctgcaga tacacttcag ttttgtttta tgcaaacatg tatacttcca tcgtgttcct 720
47 tgggctgata agcattgatc gctatctgaa ggtgggtcaag ccatttgggg actctcggat 780
48 gtacagcata accttcacga aggttttatc tgtttggtt tgggtgatca tggctgtttt 840
49 gtctttgcca aacatcatcc tgacaaatgg tcagccaaca gaggacaata tccatgactg 900
50 ctcaaaactt aaaagtcctt tgggggtcaa atggcatacg gcagtcacct atgtgaacag 960
51 ctgcttggtt gtggccgtgc tggtgattct gatcggatgt tacatagcca tatccaggta 1020
52 catccacaaa tccagcaggc aattcataag tcagtcaagc cgaaagcgaa aacataacca 1080
53 gagcatcagg gttgtgtggt ctgtgttttt tacctgcttt ctaccatata acttggtgcag 1140
54 aattcctttt acttttagtc acttagacag gcttttagat gaatctgcac aaaaaatcct 1200
55 atattactgc aaagaaatta cacttttctt gtctgcgtgt aatgtttgcc tggatccaat 1260

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56 aatttacttt ttcatgtgta ggtcattttc aagaaggctg ttcaaaaaat caaatatcag 1320
57 aaccaggagt gaaagcatca gactactgca aagtgtgaga agatcggaag ttcgcatata 1380
58 ttatgattac actgatgtgt aggcctttta ttgtttgttg gaatcgatat gtacaaagtg 1440
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62 <210> SEQ ID NO: 2

63 <211> LENGTH: 1077

64 <212> TYPE: DNA

65 <213> ORGANISM: Homo sapiens

67 <400> SEQUENCE: 2

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68 atgggggttca acttgacgct tgcaaaatta ccaataaacg agctgcacgg ccaagagagt 60
69 cacaattcag gcaacaggag cgacgggcca ggaaagaaca ccacccttca caatgaattt 120
70 gacacaattg tcttgccggt gctttatctc attatatttg tggcaagcat cttgctgaat 180
71 ggttttagcag tgtggatctt cttccacatt aggaataaaa ccagcttcat attctatctc 240
72 aaaaacatag tggttgcaga cctcataatg acgtgacat ttccatttcg aatagtccat 300
73 gatgcaggat ttggaccttg gtacttcaag tttattctct gcagatacac ttcagttttg 360
74 ttttatgcaa acatgtatac ttccatcgctg ttccttgggc tgataagcat tgatcgctat 420
75 ctgaagggtg tcaagccatt tggggactct cggatgtaca gcataacctt cacgaaggtt 480
76 ttatctgttt gtgtttgggt gatcatggct gttttgtctt tgccaaacat catcctgaca 540
77 aatggctcagc caacagagga caatatccat gactgctcaa aacttaaaag tcctttgggg 600
78 gtcaaatggc atacggcagt cacctatgtg aacagctgct tgtttgtggc cgtgctggtg 660
79 attctgatcg gatgttacat agccatatcc aggtacatcc acaaaccag caggcaattc 720
80 ataagtcagt caagccgaaa gcgaaaacat aaccagagca tcagggttgt tgtggctgtg 780
81 ttttttacct gctttctacc atatcacttg tgcagaattc cttttacttt tagtcaacta 840
82 gacaggcttt tagatgaatc tgcacaaaaa atcctatatt actgcaaaga aattacactt 900
83 ttcttgtctg cgtgtaatgt ttgcctggat ccaataattt actttttcat gtgtaggtca 960
84 ttttcaagaa ggctgttcaa aaaatcaaat atcagaacca ggagtgaag catcagatca 1020
85 ctgcaaagtg tgagaagatc ggaagttcgc atatattatg attacactga tgtgtag 1077

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88 <210> SEQ ID NO: 3

89 <211> LENGTH: 358

90 <212> TYPE: PRT

91 <213> ORGANISM: Homo sapiens

93 <400> SEQUENCE: 3

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94 Met Gly Phe Asn Leu Thr Leu Ala Lys Leu Pro Asn Asn Glu Leu His
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97 Gly Gln Glu Ser His Asn Ser Gly Asn Arg Ser Asp Gly Pro Gly Lys
98   20           25           30
100 Asn Thr Thr Leu His Asn Glu Phe Asp Thr Ile Val Leu Pro Val Leu
101   35           40           45
103 Tyr Leu Ile Ile Phe Val Ala Ser Ile Leu Leu Asn Gly Leu Ala Val
104   50           55           60
106 Trp Ile Phe Phe His Ile Arg Asn Lys Thr Ser Phe Ile Phe Tyr Leu
107   65           70           75           80
109 Lys Asn Ile Val Val Ala Asp Leu Ile Met Thr Leu Thr Phe Pro Phe
110   85           90           95
112 Arg Ile Val His Asp Ala Gly Phe Gly Pro Trp Tyr Phe Lys Phe Ile
113   100          105          110
115 Leu Cys Arg Tyr Thr Ser Val Leu Phe Tyr Ala Asn Met Tyr Thr Ser
116   115          120          125
118 Ile Val Phe Leu Gly Leu Ile Ser Ile Asp Arg Tyr Leu Lys Val Val

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119      130      135      140
121 Lys Pro Phe Gly Asp Ser Arg Met Tyr Ser Ile Thr Phe Thr Lys Val
122 145      150      155      160
124 Leu Ser Val Cys Val Trp Val Ile Met Ala Val Leu Ser Leu Pro Asn
125      165      170      175
127 Ile Ile Leu Thr Asn Gly Gln Pro Thr Glu Asp Asn Ile His Asp Cys
128      180      185      190
130 Ser Lys Leu Lys Ser Pro Leu Gly Val Lys Trp His Thr Ala Val Thr
131      195      200      205
133 Tyr Val Asn Ser Cys Leu Phe Val Ala Val Leu Val Ile Leu Ile Gly
134      210      215      220
136 Cys Tyr Ile Ala Ile Ser Arg Tyr Ile His Lys Ser Ser Arg Gln Phe
137 225      230      235      240
139 Ile Ser Gln Ser Ser Arg Lys Arg Lys His Asn Gln Ser Ile Arg Val
140      245      250      255
142 Val Val Ala Val Phe Phe Thr Cys Phe Leu Pro Tyr His Leu Cys Arg
143      260      265      270
145 Ile Pro Phe Thr Phe Ser His Leu Asp Arg Leu Leu Asp Glu Ser Ala
146      275      280      285
148 Gln Lys Ile Leu Tyr Tyr Cys Lys Glu Ile Thr Leu Phe Leu Ser Ala
149      290      295      300
151 Cys Asn Val Cys Leu Asp Pro Ile Ile Tyr Phe Phe Met Cys Arg Ser
152 305      310      315      320
154 Phe Ser Arg Arg Leu Phe Lys Lys Ser Asn Ile Arg Thr Arg Ser Glu
155      325      330      335
157 Ser Ile Arg Ser Leu Gln Ser Val Arg Arg Ser Glu Val Arg Ile Tyr
158      340      345      350
160 Tyr Asp Tyr Thr Asp Val
161      355

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164 <210> SEQ ID NO: 4

165 <211> LENGTH: 1160

166 <212> TYPE: DNA

167 <213> ORGANISM: Mus musculus

169 <400> SEQUENCE: 4

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171 cacactgcaa acagcacaag tgagggacat gggaagaact ctaccctgca caacaaattt 120
172 gacaccatca tcttgccagt gctttaccta gttatctttg tggcaagcat cctgctgaac 180
173 ggtctggccg tgtggatctt cttccacatt cggaataaaa ccagcttcat attttatctc 240
174 aaaaatatag tggtagctga cctcatcatg accctgacat tcccattccg aatagtcctg 300
175 gatgcaggat tcggaccttg gtacttcgag tttatcctct gcagatacac ctcagttttg 360
176 ttctatgcaa acatgtatac atctatcgtg tttcttgggc tgatcagtgt tgatcggtat 420
177 ctaaagggtg taaagccctt tggtagctct cgcattgtaca gcataacctt caccaaagtt 480
178 ttatcagttt gtgtttgggt gatcatggct attctgtcct tgccaaacat catactgact 540
179 aatgggcagc caactaagga aaatattcat gactgcatga aactcaaaag tccgctggga 600
180 gccaaagtggc atatggctgt cacctatgtg gacagctgtt tgtttgtggc cgtgctgggt 660
181 atcctgattg gatgctacat agccatctcc agatacatcc acaaatccag caggcaattc 720
182 ataagccaat cgagccggaa gcgaaagcac aaccagagca tccgcgtggg cgtggctgtg 780
183 ttttttacct gcttctccc gtatcacttg tgcagaatcc cctttacctt cagtaactta 840
184 gacaggcttc tggatgaatc agcacataaa atcctctact attgcaaaga aatgacactt 900

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185 ttcttgtctg cgtgcaacgt gtgcctggat ccgataattt attttttcat gtgtaagtca 960
186 ttttcaagaa ggttattcaa gaaatcaaac ataagaacca ggagcgaaag catcagggtcg 1020
187 ctgcaaagcg tccgaagatc agaagtgcgc atctattatg actacactga tgtgtaagga 1080
188 ctagaggcca gggacccttt tctattggaa tcagtatgta aaagagtgta aataaatgtt 1140
189 tctttttatt atcttggtg 1160
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193 <211> LENGTH: 358
194 <212> TYPE: PRT
195 <213> ORGANISM: Mus musculus
197 <400> SEQUENCE: 5
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199 1 5 10 15
201 Ser Gln Ala Ser His Thr Ala Asn Ser Thr Ser Glu Gly His Gly Lys
202 20 25 30
204 Asn Ser Thr Leu His Asn Lys Phe Asp Thr Ile Ile Leu Pro Val Leu
205 35 40 45
207 Tyr Leu Val Ile Phe Val Ala Ser Ile Leu Leu Asn Gly Leu Ala Val
208 50 55 60
210 Trp Ile Phe Phe His Ile Arg Asn Lys Thr Ser Phe Ile Phe Tyr Leu
211 65 70 75 80
213 Lys Asn Ile Val Val Ala Asp Leu Ile Met Thr Leu Thr Phe Pro Phe
214 85 90 95
216 Arg Ile Val Arg Asp Ala Gly Phe Gly Pro Trp Tyr Phe Glu Phe Ile
217 100 105 110
219 Leu Cys Arg Tyr Thr Ser Val Leu Phe Tyr Ala Asn Met Tyr Thr Ser
220 115 120 125
222 Ile Val Phe Leu Gly Leu Ile Ser Val Asp Arg Tyr Leu Lys Val Val
223 130 135 140
225 Lys Pro Phe Gly Asp Ser Arg Met Tyr Ser Ile Thr Phe Thr Lys Val
226 145 150 155 160
228 Leu Ser Val Cys Val Trp Val Ile Met Ala Ile Leu Ser Leu Pro Asn
229 165 170 175
231 Ile Ile Leu Thr Asn Gly Gln Pro Thr Lys Glu Asn Ile His Asp Cys
232 180 185 190
234 Met Lys Leu Lys Ser Pro Leu Gly Ala Lys Trp His Met Ala Val Thr
235 195 200 205
237 Tyr Val Asp Ser Cys Leu Phe Val Ala Val Leu Val Ile Leu Ile Gly
238 210 215 220
240 Cys Tyr Ile Ala Ile Ser Arg Tyr Ile His Lys Ser Ser Arg Gln Phe
241 225 230 235 240
243 Ile Ser Gln Ser Ser Arg Lys Arg Lys His Asn Gln Ser Ile Arg Val
244 245 250 255
246 Val Val Ala Val Phe Phe Thr Cys Phe Leu Pro Tyr His Leu Cys Arg
247 260 265 270
249 Ile Pro Phe Thr Phe Ser Asn Leu Asp Arg Leu Leu Asp Glu Ser Ala
250 275 280 285
252 His Lys Ile Leu Tyr Tyr Cys Lys Glu Met Thr Leu Phe Leu Ser Ala
253 290 295 300
255 Cys Asn Val Cys Leu Asp Pro Ile Ile Tyr Phe Phe Met Cys Lys Ser

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256 305          310          315          320
258 Phe Ser Arg Arg Leu Phe Lys Lys Ser Asn Ile Arg Thr Arg Ser Glu
259          325          330          335
261 Ser Ile Arg Ser Leu Gln Ser Val Arg Arg Ser Glu Val Arg Ile Tyr
262          340          345          350
264 Tyr Asp Tyr Thr Asp Val
265          355
268 <210> SEQ ID NO: 6
269 <211> LENGTH: 384
270 <212> TYPE: PRT
271 <213> ORGANISM: Artificial Sequence
273 <220> FEATURE:
274 <223> OTHER INFORMATION: Description of Artificial Sequence: Fusion protein
275 of human Mowgli (SEQ ID NO: 3) with V5 and His
276 tags at C-terminal end
278 <400> SEQUENCE: 6
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280 1 5 10 15
282 Gly Gln Glu Ser His Asn Ser Gly Asn Arg Ser Asp Gly Pro Gly Lys
283 20 25 30
285 Asn Thr Thr Leu His Asn Glu Phe Asp Thr Ile Val Leu Pro Val Leu
286 35 40 45
288 Tyr Leu Ile Ile Phe Val Ala Ser Ile Leu Leu Asn Gly Leu Ala Val
289 50 55 60
291 Trp Ile Phe Phe His Ile Arg Asn Lys Thr Ser Phe Ile Phe Tyr Leu
292 65 70 75 80
294 Lys Asn Ile Val Val Ala Asp Leu Ile Met Thr Leu Thr Phe Pro Phe
295 85 90 95
297 Arg Ile Val His Asp Ala Gly Phe Gly Pro Trp Tyr Phe Lys Phe Ile
298 100 105 110
300 Leu Cys Arg Tyr Thr Ser Val Leu Phe Tyr Ala Asn Met Tyr Thr Ser
301 115 120 125
303 Ile Val Phe Leu Gly Leu Ile Ser Ile Asp Arg Tyr Leu Lys Val Val
304 130 135 140
306 Lys Pro Phe Gly Asp Ser Arg Met Tyr Ser Ile Thr Phe Thr Lys Val
307 145 150 155 160
309 Leu Ser Val Cys Val Trp Val Ile Met Ala Val Leu Ser Leu Pro Asn
310 165 170 175
312 Ile Ile Leu Thr Asn Gly Gln Pro Thr Glu Asp Asn Ile His Asp Cys
313 180 185 190
315 Ser Lys Leu Lys Ser Pro Leu Gly Val Lys Trp His Thr Ala Val Thr
316 195 200 205
318 Tyr Val Asn Ser Cys Leu Phe Val Ala Val Leu Val Ile Leu Ile Gly
319 210 215 220
321 Cys Tyr Ile Ala Ile Ser Arg Tyr Ile His Lys Ser Ser Arg Gln Phe
322 225 230 235 240
324 Ile Ser Gln Ser Ser Arg Lys Arg Lys His Asn Gln Ser Ile Arg Val
325 245 250 255
327 Val Val Ala Val Phe Phe Thr Cys Phe Leu Pro Tyr His Leu Cys Arg

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VERIFICATION SUMMARY

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TIME: 15:40:50

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